

FIG. 4

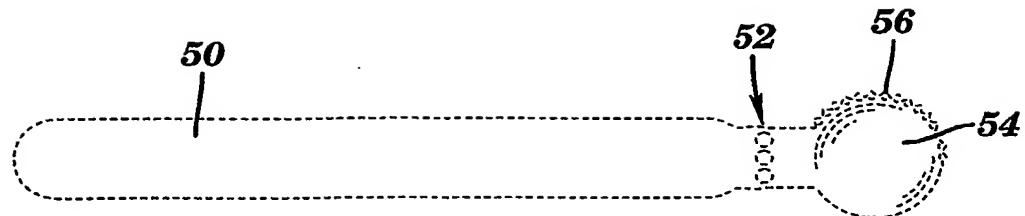


FIG. 5A

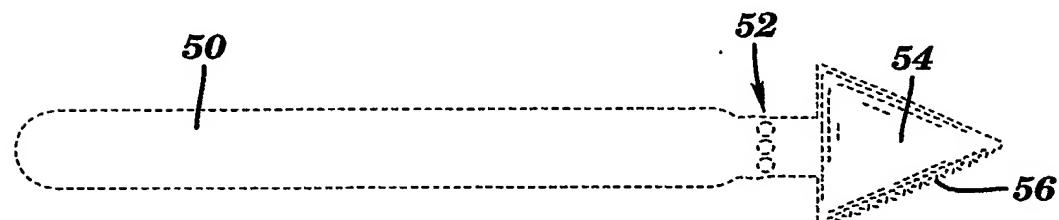


FIG. 5B

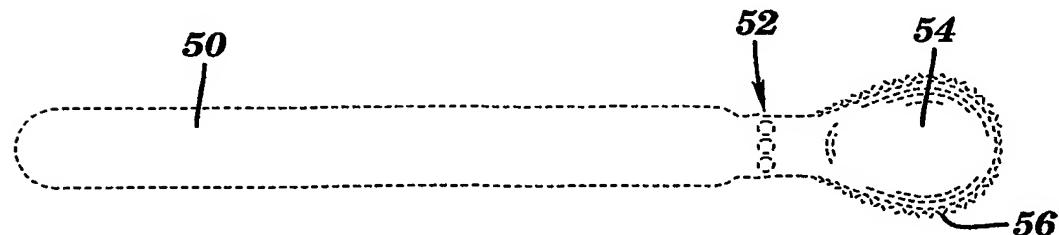
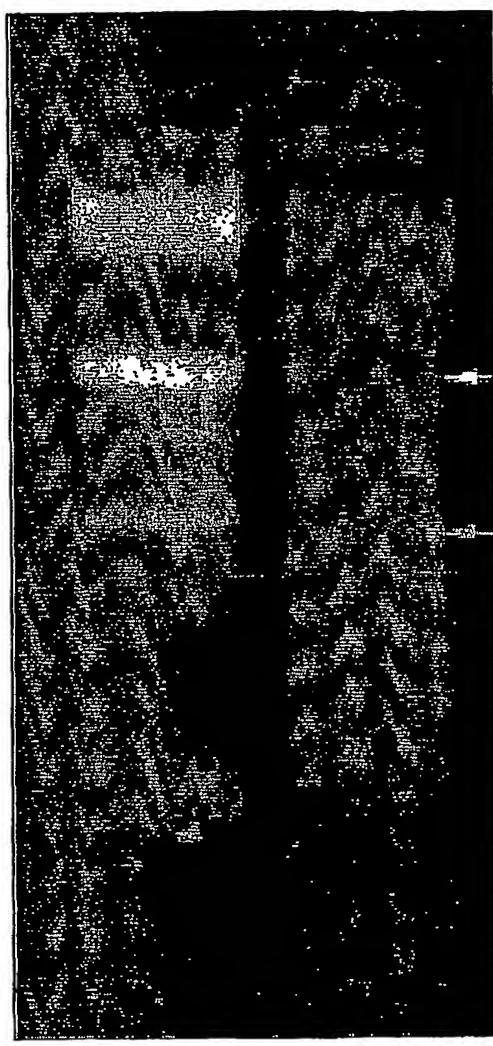


FIG. 5C



LANE 1

LANE 2

FIG. 6

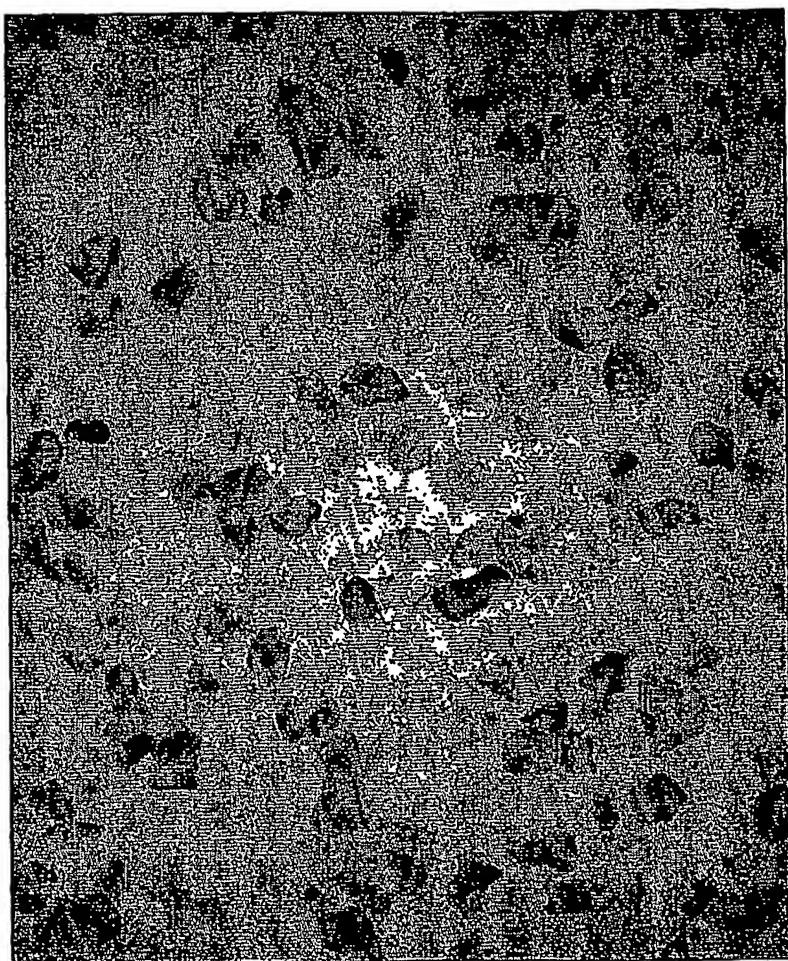


FIG. 7

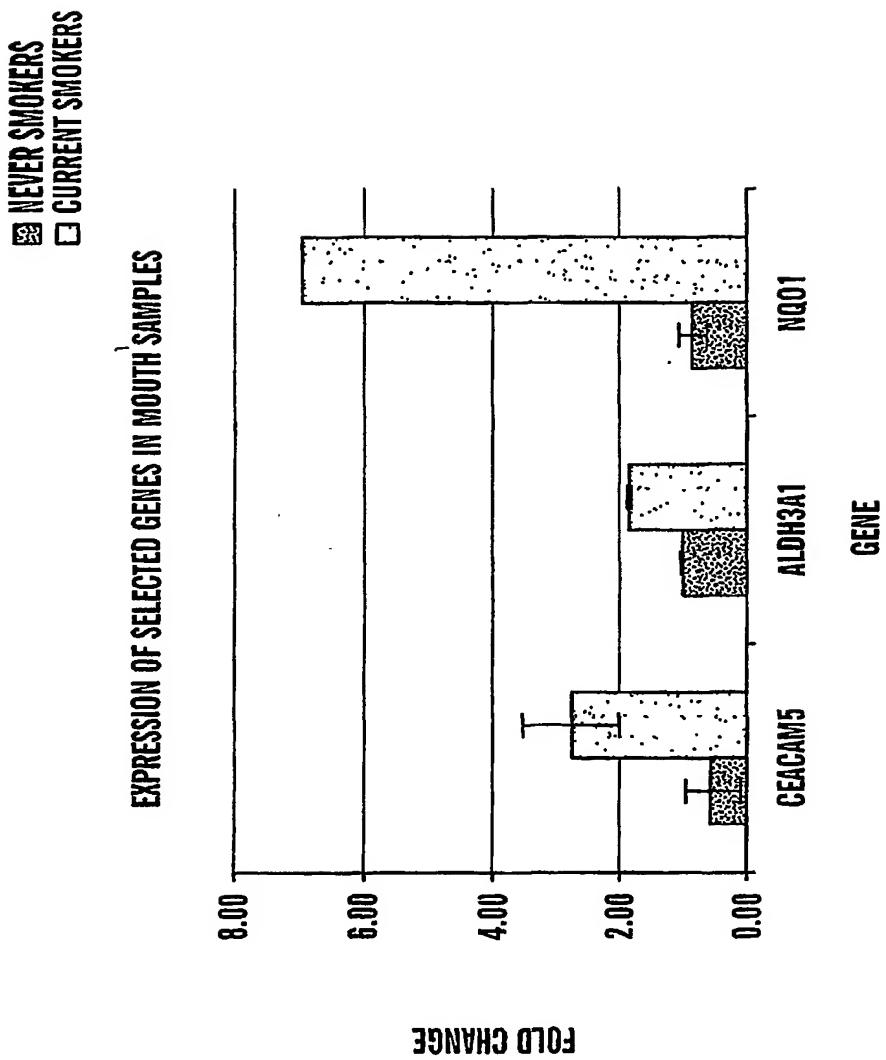


FIG. 8A

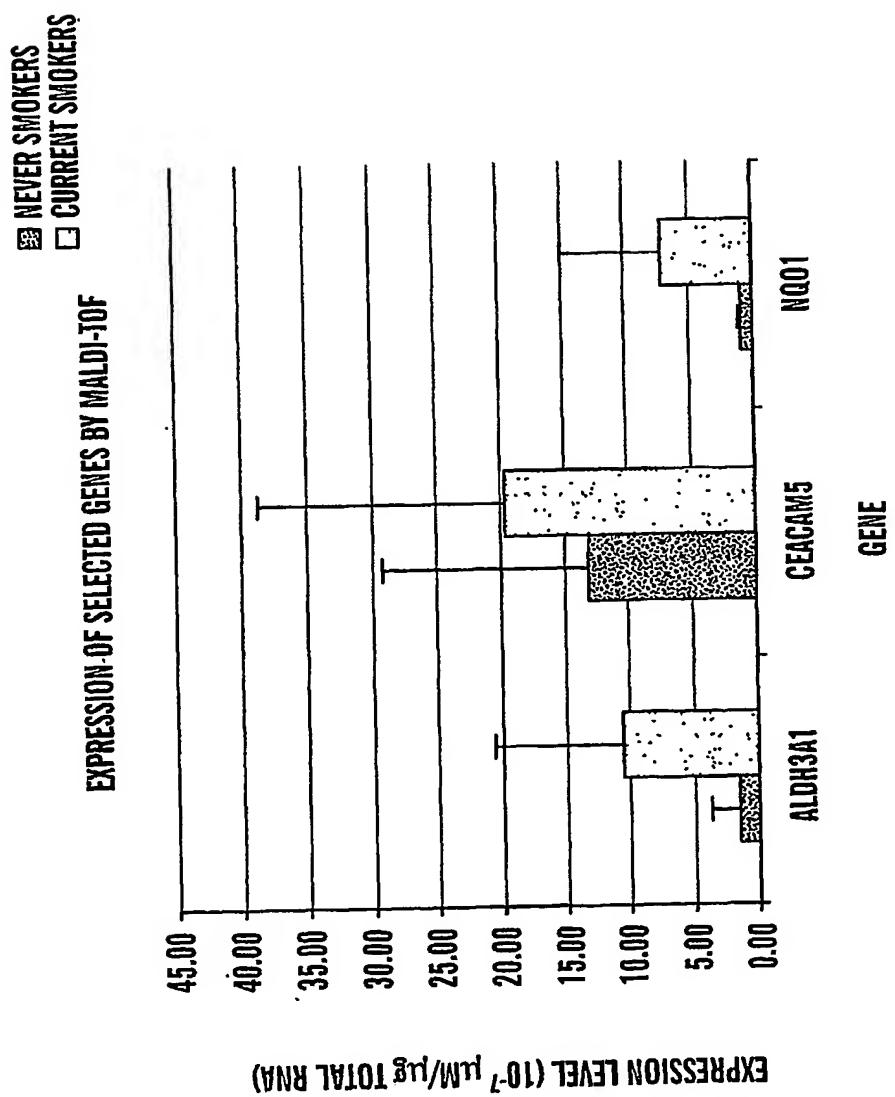
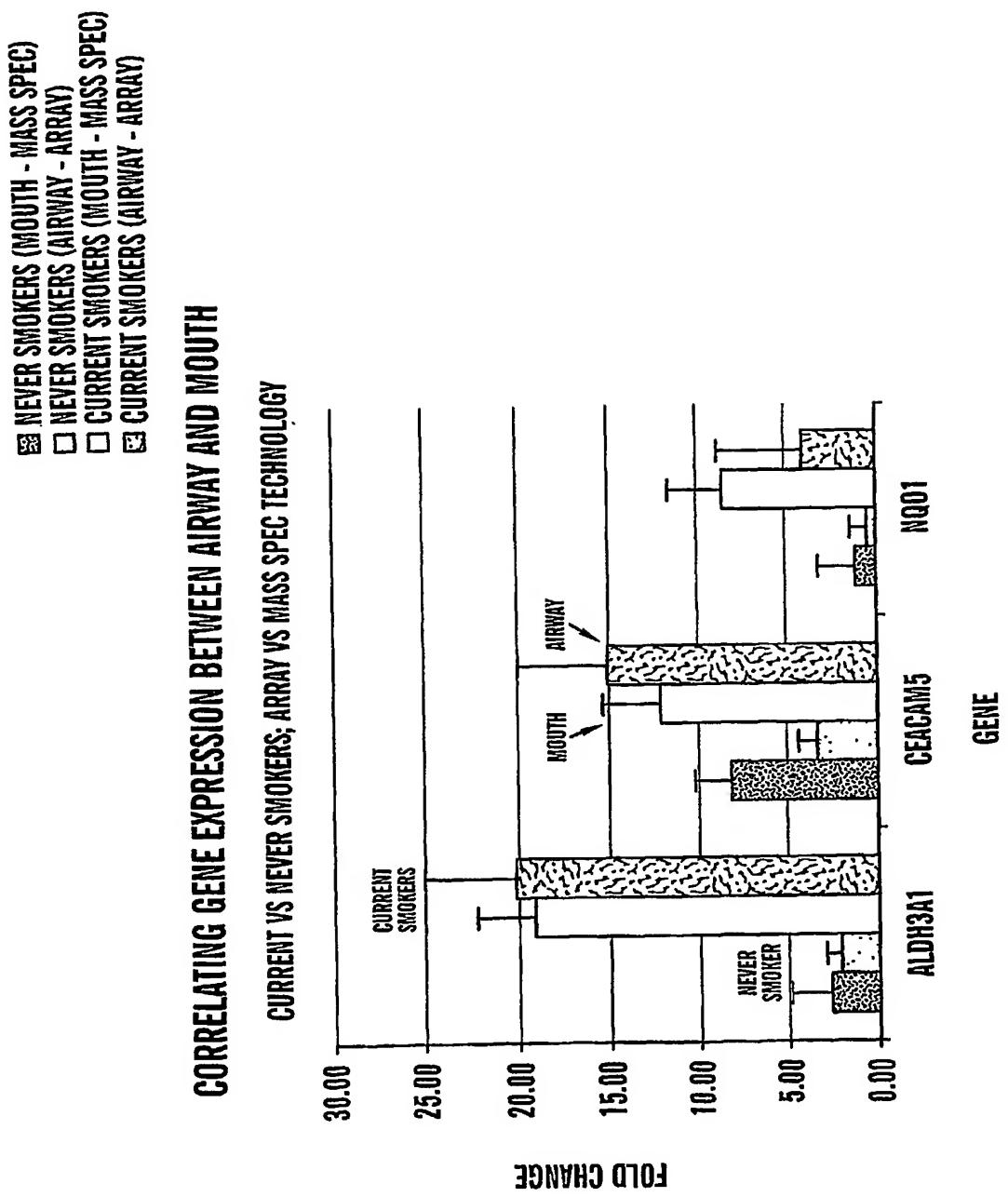
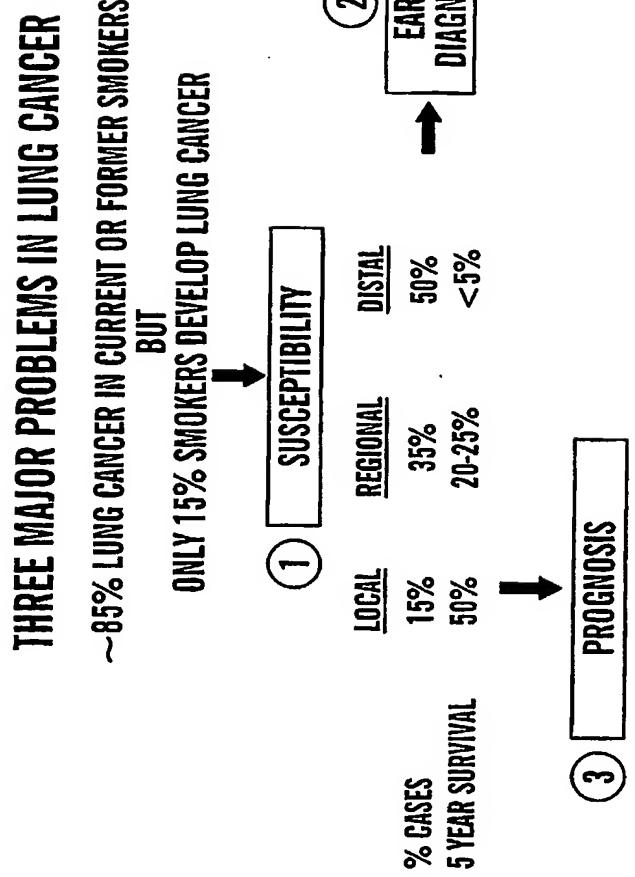


FIG. 8B



**FIG. 10**

Affymetrix ID	GENBANK ID	HUGO ID	GO ID	Current/Never smoker p-value	Current/Never smoker Ratio	CHROMOSOME LOCATION	GENBANK DESCRIPTION
220562_at	NM_017781.1	FLJ20359	6118	1.2E-05	0.414665	7p22.3	hypothetical protein FLJ20359
219410_at	NM_018004.1	FLJ10134	16021	0.00044	0.435962	3q12.3	hypothetical protein FLJ10134
	AF078844.1	MT1F	5737	2.4E-05	0.469865	16q13	metallothionein 1F (functional)
	NM_005951.1	MT1H	46872	3.4E-05	0.481306	16q13	metallothionein 1H
	BC005894.1	FM02	6118	0.0005	0.487651	1q23-q25	flavin containing monooxygenase 2
							"cytochrome P450, family 2, subfamily A, polypeptide 6"
	AF182275.1	CYP2A6	6118	0.00041	0.509566	19q13.2	metallothionein 1F (functional)
	BF246115	MT1F	5737	1.7E-07	0.523748	16q13	metallothionein 1X
	NM_005952.1	MT1X	9634	6.3E-06	0.546094	16q13	metallothionein 1G
	NM_005950.1	MT1G	46872	1.8E-06	0.554828	16q13	"creatinine kinase, brain"
	NM_001823.1	CKB	5737	na	0.567052	14q32	hydroxyprostaglandin dehydrogenase 15-(NAD)
	NM_000860.1	HPGD	8152	0.00061	0.569176	4q34-q35	integral membrane protein 2A
	AL021786	ITM2A	16021	7.1E-05	0.578361	Xq13.3-Xq21.2	sorbitol dehydrogenase
	L29008.1	SORD	6060	..	0.00036	15q15.3	keratin 15
	NM_002275.1	KRT15	8544	..	0.00056	17q21.2	hypothetical gene supported by S68948
	AF333388.1	na		3.9E-05	0.585312	1q42.3	heat shock 70kDa protein 2
	U56725.1	HSPA2	7286	4.2E-07	0.586718	14q24.1	metallothionein 1F (functional)
	M10943	MT1F	5737	5.1E-07	0.596388	16q13	

BF217861	MTIE	6823	0.00038	0.596821	16q13
AF052094.1	EPAS1		1.5E-05	0.613378	2p21-p16
396_f_at	EPOR MTIX	7165 5737	0.00035 2.3E-06	0.614894 0.631575	19p13.3-p13.2 16q13
AF114012.1 NM_005953.1 AL046979	TNFSF13 MT2A TNS	6878	2.3E-05 5E-05 0.00018	0.674117 0.675192 0.679047	17p13.1 16q13 2q35-q36
205752_s_at	NM_000851.1	GSTM5	6803	0.00019	0.688656
AB017546	PEX14	5777	0.00045	0.696156	1p13.3
NM_006312.1	NCOR2	3677	3.3E-05	0.703316	1p36.22
NM_006314.1	CNK1	7242	0.00069	0.706868	12q24
AB014605.1	AIP1	7242	0.00093	0.7116147	17p11.2
NM_031283.1	TCFL1	6355	1.3E-05	0.719296	7q21
AB007857 NM_001888.1	KIAA0397 CRYM	7601	0.00019 0.00085	0.721366 0.727149	17p13.3 16p13.11-p12.3
NM_005769.1	CHST4	8146	0.00095	0.73709	16q22.2
					16q22.2
					(N-acetyl)glucosamine 6-O)

FIG. 11
(cont'd.)

BC006230.1 NM_018555.2	MGLL ZNF463	6954 6355	6.3E-06 0.00041	0.739267 0.753755	3q21.3 19q13.3-q13.4
NM_015001.1	SHARP	3676	0.00016	0.766024	1p36.33-p36.11
NM_016605.1	C5orf6	5634	0.00032	0.795545 5q31	
AW001443 AA046650	GGA1 HRHFB2122	6886 30047	0.00097 0.00047	0.799768 0.806466	22q13.31 22q13.1
Z97056	KDELR3		0.00088	0.835711	22q13.1
BC001049.1	UFDIL	6511	0.0007	1.198875	22q11.21
NM_015523.1	DKFZP566E144	9117	5.2E-05	1.200265	11q23.1-q23.2
NM_006694.1	JTB	7048	0.00044	1.201571	1q21
NM_030796.1	DKFZP564K0822		0.00043	1.209285	7p11.2
AF217514.1	C20orf111		0.00014	1.219712	20q13.11
AF027205.1	SPINT2	6928	0.00063	1.220877	19q13.1
209679_s_at	LOC57228 GUK1 Clorf8	6183 16021	0.00051 9.2E-05 0.00057	1.2232881 1.234086 1.242047	12q13.13 1q32-q41 1p36-p31

FIG. 11
(cont'd.)

MR4859.1	CANX	9306	0.00038	1.243131	5q35	open reading frame 8 calnexin "FK506 binding protein 1A, 12kDa" hypothetical protein LOC92482 "CAP, adenylate cyclase-associated protein 1 (yeast)" DKFZP434J214 protein
NM_000801.1	FKBP1A	6457	0.00038	1.247517	20p13	ribophorin II protein expressed in thyroid
AV706096	LOC92482	6915	0.00019	1.248195	10q25.3	sequestosome 1 "proteasome (prosome, macropain) subunit, beta type, 5" "thioredoxin-like, 32kDa" "transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)" "signal sequence receptor, delta (translocon-associated protein delta)" thioredoxin domain containing 5 "coatomer protein complex, subunit
NM_006367.2	CAP1	7190	0.00052	1.256141	1p34.2	
AL556438	DKFZP434J214	6464	0.00097	1.257122	3q25.31	
BC033560.1	RPN2		0.00045	1.257736	20q12;q13.1	
NM_014297.1	YFI13H12		0.0002	1.260627	19q13.32	
NM_003900.1	SQSTM1	5829	0.00012	1.264144	5q35	
BC004146.1	PSMB5		3.3E-05	1.265493	14q11.2	
NM_004786.1	TXNL	7165	0.0002	1.270987	18q21.31	
203201_at	AI951720	TLE1	6355	0.00031	1.272507	9q21.32
NM_006280.1	SSR4		6886	0.00024	1.273482	Xq28
NM_030810.1	TXNDC5		6118	0.00074	1.275599	6p24.3
NM_004766.1	COPB2		6886	6.4E-05	1.278174	3q23

FIG. 11
(cont'd.)

AF139131.1	BECN1	6916	0.00087	1.28931	17q21	beta 2 (beta prime)" "beclin 1 (coiled-coil, myosin-like BCL2 interacting protein)"
NM_006827.1	TMP21	6888	0.00047	1.296788	14q24.3	transmembrane trafficking protein tumor rejection
NM_003299.1	TRA1	5524	3.1E-05	1.2999298	12q24.2-12q24.3	antigen (EP96) 1 UDP-N-acetyl-alpha- D-galactosamine: polypeptide N-
NM_020474.2	GALNT1	7157	4.3E-05	1.300002	18q12.1	acetyl galactosaminyltransferase 1 (GalNAc-T1)
NM_0053886.1	KATNB1	7049	0.00034	1.301892	16q13	katam p80 (WD repeat containing) subunit B 1 hypothetical protein
NM_024329.1	MGC4342	5509	0.00028	1.304455	1p36.13	MGC4342
NM_004817.1	TIP2	7242	0.00096	1.306517	9q13-q21	tight junction protein 2 (zona occludens 2)
AK000095.1	CHP		0.00084	1.3111387	15q13.3	calcium binding protein P22
BC000758.1	C6orf80		0.00015	1.318101	6q23.1-12q24.1	chromosome 6 open reading frame 80 Down syndrome
AB035745.1	DSCR5	16021	0.00033	1.321519	21q22.2	critical region gene 5
NM_005805.1	PSMD14	6511	0.00067	1.333381	2q24.3	"proteasome (prosome, macropain) 26S subunit, non-ATPase, 14" tumor-associated
J04152	TACSTD2	8283	0.00037	1.335595	1p32-p31	calcium signal transducer 2
NM_016021.1	UBE2J1	4840	0.00029	1.336642	6q16.1	"ubiquitin-conjugating

FIG. 11
(cont'd.)

BC004371.1	APLP2	16020	0.00026	1.342607	11q24	enzyme E2, J1 (UBC6 homolog, yeast)"
NM_004255.1	COX5A	6118	0.00011	1.346133	15q25	amyloid beta (A4) precursor-like protein 2
AI215102	RAB11A	6886	2.5E-06	1.348199	15q21.3-q22.31	cytochrome c oxidase subunit Va
J04183.1	LAMP2	5765	0.00092	1.349815	Xq24	"RAB11A, member
NM_005896.1	IDH1	6097	0.00043	1.356411	2q33.3	lysosomal-associated membrane protein 2
M97655.1	PTS	7417	2.4E-05	1.359451	11q22.3-q23.3	"isocitrate dehydrogenase 1 (NADP+), soluble"
AK024976.1	RNP24	6886	0.00018	1.362023	12q24.31	6-pyruvoyltetrahydropterin synthase
AF131820.1	GH1TM	16021	0.0005	1.362421	10q23.2	coated vesicle
NM_000202.2	IDS	5764	0.00072	1.363052	Xq28	membrane protein
NM_001177.2	ARL1	7264	0.00042	1.363278	12q23.3	growth hormone inducible transmembrane protein
211960_s_at	AK000826.1 NM_006406.1	RAB7 PRDX4	6897 7252	0.00065 2E-05	1.365319 1.368691	iduronate 2-sulfatase (Hunter syndrome)
D83485.1	GRP58	7165	0.00041	1.374384	15q15	ADP-ribosylation factor-like 1
NM_014056.1 NM_000177.1	HIG1 GSN	30041	3.4E-05 0.00026	1.384249 1.388286	1.3p21.33 9q33	"RAB7, member
						"RAS oncogene family"
						peroxiredoxin 4
						"glucose regulated protein, 58kDa"
						likely ortholog of mouse hypoxia induced gene 1
						"gelsolin"

FIG. 11
(cont'd.)

BG054844 BC001709.1	ARHE FLJ13052	7012	0.00018 2.1E-05	1.402285 1.404051	2q23.3 1p36.33-p36.21
213135_at	TIAMI HIST1H2BK	6334	7.1E-05 0.00032	1.417117 1.425082	21q22.11 6p21.33
					"Homo sapiens histone 1, H2ac, mRNA (cDNA clone IMAGE:6526471), partial cds"
AL333759	---	7001	0.0004	1.428349	---
221041_s_at	NM_012434.1	SLC17A5	6820	7.1E-05	1.428655
					"solute carrier family 17 (anion/sugar transporter), member 5"
AF004561.1 NM_014933.1 NM_003909.1	ARPC3 KIAA0905 CPNE3 CCNG2 DSG2	6928	0.00013 0.00016 0.00019 0.00013 0.00064	1.431352 1.432349 1.439945 1.444115 1.450408	12q24.11 4q21.3 8q21.2 4q21.22 18q12.1
202769_at	AW134535 BF031829				
200733_s_at	U48296.1	PTP4A1	7048	5.3E-05	1.450813
					6q12
208918_s_at 204500_s_at	NM_004776.1 BC001709.1 NM_015239.1	B4GALT5 FLJ13052 AGTPBP1	5794	0.00028 2.1E-06 7.3E-05	1.454948 1.455424 1.466039
					20q13.1-q13.2 1p36.33-p36.21 9q22.1
J02783.1	P4HB		6118	0.00011	1.472842
					17q25

FIG. 11
(*cont'd.*)

NM_020672.1	SI100A14	5509	0.00017	1.479972	1q21.1
LL527430	GSTM3	6803	0.00099	1.481409	1p13.3
NM_004753.1	SDR1	8152	1E-08	1.49171	1p36.1
NM_007011.1	ABHD2	16021	8.8E-07	1.4988	15q26.1
11539710	ABCC1	6832	9.7E-07	1.511282	16p13.1
NM_002865.1	RAB2	6886	0.00024	1.528634	8q12.1
NG288007	LYPLA1		0.00058	1.542594	8q11.23
NM_002032.1	FTH1	6826	1E-08	1.545805	11q13
NM_002885.1	RAP1GA1	7165	6.7E-05	1.549434	1p36.1-p35
NM_006729.1	DIAPH2		2.2E-05	1.549995	Xq22
AF200715.1	CED-6	6911	0.00088	1.555117	2q32.3-q33
CC005911.1	SCP2	6694	0.00044	1.562614	1p32
3F063271	GALNT3	5975		1.575931	2q24-q31
				2.4E-06	

FIG. 11
(cont'd.)

NM_014399.1	TM4SF13	5887	1.1E-06	1.577122	7p21.2
NM_005476.2	GNE	6054	0.0001	1.577697	9p13.1
NM_019094.1	NUDT4	9187	2E-08	1.583297	—
AI762113	GMDS	5975	1.1E-06	1.596075	6p25
214106_s_at	IMP12	7165	1.1E-05	1.603212	18p11.2
203126_at	NM_014214.1			8.2E-05	1.624152
	AV728268	SORLI		6.6E-05	11q23.2-q24.2
	NM_003191.1	TARS		1.7E-05	5p13.2
201263_at	LOC51186	6435		1.634697	Xq22.2
	NM_016303.1				
					35 (UDP-N-acetyl glucosamine (UDP-GlcNAc) transporter), member A3"
NM_012243.1	SLC35A3		0.00095	1.639247	1p21
AA873600	ASM3A	16787	2.5E-05	1.639892	6q22.32
W87466	LOC92689		0	1.651404	4p14
213624_at	NM_016315.1	CED-6	6911	0.00019	1.660108
	AF247704.1	NKX3-1		3E-05	2q32.3-q33
	NM_001072.1	UGT1A10		1.4E-07	1.677318
					8p21
					1.69228
					2q37

204970_s_at	NM_002359.1 NM_005980.1	MAFG S100P	6355 5515	1.2E-07 2.8E-06	1.704793 1.712088	17q25 4p16
206515_at	NM_000896.1 L19184.1	CYP4F3 PRDX1	6118 8283	0.00038 7.7E-07	1.745995 1.760529	19p13.2 1p34.1
NM_002966.1	S100A10		7165	1.2E-05	1.765162	1q21
NM_021027.1	UGT1A10		8152	0	1.769976	2q37
NM_017423.1	GALNT7		5975	6E-08	1.772633	4q31.1
BF676980	GCLC		6534	1.7E-05	1.782371	6p12
NM_001500.1	GMDS		5975	5.4E-06	1.821792	6p25
217755_at	NM_016185.1 AA083483	HNI FTH1		9E-08 1.1E-05	1.842243 1.848912	17q25.2 11q13
AL117536.1		na		1.4E-05	1.875907	Xq28
M92934.1 M63310.1	CTGF ANXA3		1558 5737	2.8E-06 2.5E-07	1.907245 1.922919	6q23.1 4q13-q22
209369_at						growth factor annexin A3

FIG. 11 (cont'd.)

203963_at	NM_000463.1 NM_001218.2	UGT1A10 CA12	16758 6730	1E-08 0	1.977759 2.054255	2q37 15q22
219928_s_at	NM_012189.1	CABYR	8603	1.7E-05	2.069324	18q11.2
	BC005008.1 NM_003330.1	CEACAM6 TXNRD1	7165 6118	6.1E-05 3E-08	2.09128 2.091704	19q13.2 12q23-q24.1
	NM_002631.1	PGD	9051	9E-08	2.09455	1p36.3-p36.13
	NM_002061.1 NM_006755.1	GCLM TALD01	6534 5975	2.6E-07 0	2.132184 2.147132	1p22.1 11p15.5-p15.4
						carinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
						thioredoxin reductase 1 phosphogluconate dehydrogenase "glutamate-cysteine ligase, modifier subunit" transaldolase 1 carinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
	M18728.1 NM_005213.1 U73945.1 AF313911.1	CEACAM6 CSTA DEFB1 TXN	7165 4869 6805 7165	1.5E-07 0.00033 0.00049 0	2.167528 2.168054 2.185117 2.209985	19q13.2 3q21 8p23.2-p23.1 9q31
221841_s_at	BF514079	KLF4		9.3E-06	2.247407	9q31
	NM_006470.1 NM_014467.1	TRIM16 SRPUL	5737 6118	3E-08 0	2.279802 2.330972	17p11.2 Xq21.33-q23
205499_at					1E-08 0	2.410897 2.718782
204058_at 204059_s_at	AL049699 NM_002395.2	ME1 ME1	6099 6099		6q12 6q12	"cytosolic" "malic enzyme 1," "malic enzyme 1,"

FIG. 11
(cont'd.)

209351_at	BC002690.1	KRT14	7148	0.00058	2.8239	17q12-q21	NADP(+) -dependent, cytosolic" "keratin 14 (epidermolysis bullosa simplex, Dowling-Meara, Koebner)" transmembrane 4
209386_at	AI346835	TM4SF1	5887	0.00012	2.998073	3q21-q25	superfamily member 1 "aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)- hydroxysteroid dehydrogenase)" "NAD(P)H dehydrogenase, quinone 1" claudin 10
	NM_001353.2	AKR1C1	6805	2.9E-05	3.186574	10p15-p14	"aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)- hydroxysteroid dehydrogenase)" "NAD(P)H dehydrogenase, quinone 1" claudin 10
	BC000906.1	NQO1	6118	0	3.61596	16q22.1	
	NM_006984.1	CLDN10	7155	1E-08	3.842393	13q31-q34	
	S68290.1	AKR1C1	6805	3.8E-07	3.859724	10p15-p14	"aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)" glutathione peroxidase 2 (gastrointestinal)
	M33376.1	AKR1C2		9E-08	4.050088	10p15-p14	
	NM_002083.1	GPX2	6979	0	4.247676	14q24.1	
	NM_000903.1	NQO1	6118	0	4.278763	16q22.1	
	NM_000691.1	ALDH3A1	6081	0	7.135677	17p11.2	"aldehyde dehydrogenase

FIG. 11
(cont'd.)

NADP(+) -dependent, cytosolic"							
"keratin 14							
(epidermolysis bullosa simplex, Dowling-Meara, Koebner)"							
transmembrane 4							
superfamily member 1							
family 1, member C1							
"aldo-keto reductase (dihydrodiol dehydrogenase 1;							
20-alpha (3-alpha)-hydroxysteroid dehydrogenase)"							
"NAD(P)H dehydrogenase, quinone 1"							
claudin 10							
"aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)"							
"aldo-keto reductase family 1, member C2 (dihydrodiol dehydrogenase 2; bile acid binding protein; 3-alpha hydroxysteroid dehydrogenase, type III)"							
glutathione peroxidase 2 (gastrointestinal)							
"NAD(P)H dehydrogenase, quinone 1"							
"aldehyde dehydrogenase							
BC002690.1	KRT14	7148	0.00058	2.8239	17q12-q21		
AI346835	TM4SF1	5887	0.00012	2.998073	3q21-q25		
NM_001353.2	AKR1C1	6805	2.9E-05	3.186574	10p15-p14		
BC000906.1	NQO1	6118	0	3.61596	16q22.1		
NM_006984.1	CLDN10	7155	1E-08	3.842293	13q31-q34		
S68290.1	AKR1C1	6805	3.8E-07	3.859724	10p15-p14		
M33376.1	AKR1C2		9E-08	4.050088	10p15-p14		
NM_002083.1	GPX2	6979	0	4.247676	14q24.1		
NM_000903.1	NQO1	6118	0	4.278763	16q22.1		
NM_000691.1	ALDH3A1	6091	0	7.135677	17p11.2		

SUBSTITUTE SHEET (RULE 26)

NM_004363.1	CEACAM5	5887	1.5E-05	7.574469	19q13.1-q13.2	3 family, member A1" carcinoembryonic antigen-related cell adhesion molecule 5
NM_000104.2	CYP1B1	6118	3.6E-05	8.874184	2p21	"cytochrome P450, family 1, subfamily B, polypeptide 1" "aldo-keto reductase family 1, member B10 (aldose reductase)"
NM_020299.1	AKR1B10	4033	0.0005	25.99183	7q33	

FIG. 11
(cont'd.)

Affymetrx	GENBANK	HUGO	GO	Smoker/		Smoker/ Non-Smoker Expression Ratio	
				Smoker/			
				Non-smoker	p-value		
ID	ID	ID	ID				
205680_at	NM_002425	MMP10	30574		4E-08	0.397067	
210524_x_at	NM_007372	MT1F	5737		7.81E-06	0.527231	
208581_x_at	NM_005952	MT1X	9634		3.1E-07	0.553203	
211538_s_at	NM_021979	HSPA2	7286		1.6E-07	0.594697	
204745_x_at	NM_005950	MT1G	46872		1.47E-06	0.600768	
217165_x_at	M10943	MT1F	5737		3.1E-07	0.617346	
221016_s_at	NM_031283	TCF-3	6355		1.9E-07	0.69786	
211026_s_at	NM_007283	MGLL	6954		6.72E-06	0.757342	
200599_s_at	NM_003299	TRA1	5524		1.6E-06	1.28607	
200863_s_at	NM_004663	RAB11A	6886		1.51E-05	1.287348	
201923_at	NM_006406	PRDX4	7252		1.46E-05	1.31812	
208918_s_at	NM_023018	FLJ13052			1.63E-05	1.357851	
208919_s_at	NM_023018	FLJ13052			2.38E-06	1.377841	
202481_at	NM_004753	SDR1	8152		3.25E-06	1.386494	
204500_s_at	NM_015239	AGTPBP1			1.73E-05	1.434528	
206302_s_at	NM_019094	NUDT4	9187		9.8E-07	1.438227	
200748_s_at	NM_002032	FTH1	6826		0	1.482301	
203397_s_at	NM_004482	GALNT3	5975		1.25E-05	1.494527	
214106_s_at	NM_001500	GMDS	5975		6.9E-07	1.505996	
201263_at	NM_003191	TARS	6435		2.06E-05	1.534493	
204970_s_at	NM_002359	MAFG	6355		1.06E-05	1.54913	
200872_at	NM_002966	S100A10	7165		1.83E-05	1.599726	
208680_at	NM_002574	PRDX1	8283		4.2E-07	1.624891	
218313_s_at	NM_017423	GALNT7	5975		1.1E-07	1.636258	
201431_s_at	NM_001387	DPYSL3	7165		5E-07	1.7288	
217755_at	NM_016185	HN1			2E-08	1.732046	
203963_at	NM_001218	CA12	6730		5.4E-07	1.751505	

FIG. 12

202923_s_at	NM_001498	GCLC	6534	1.7E-07	1.773281
204875_s_at	NM_001500	GMDS	5975	8E-08	1.830569
201266_at	NM_003330	TXNRD1	6118	3E-08	1.865058
201118_at	NM_002631	PGD	9051	2.3E-07	1.866207
209369_at	NM_005139	ANXA3	5737	2.5E-07	1.872862
203925_at	NM_002061	GCLM	6534	1.54E-06	1.87522
211657_at	M18728.1	CEACAM6	7165	2E-08	1.925775
208864_s_at	NM_003329	TXN	7165	0	1.961322
201463_s_at	NM_006755	TALDO1	5975	0	1.974839
203757_s_at	NM_002483	CEACAM6	7165	1.65E-06	1.987336
205499_at	NM_014467	SRPUL	6118	3E-08	2.038793
204341_at	NM_006470	TRIM16	5737	0	2.048029
204058_at	AL049699	ME1	6099	0	2.104857
221841_s_at	NM_004235	---		9.18E-06	2.208524
204059_s_at	NM_002395	ME1	6099	0	2.414563
204151_x_at	NM_001353	AKR1C1	6805	2.93E-06	2.854519
210519_s_at	BC000906.1	NQO1	6118	0	3.076752
216594_x_at	S68290.1	AKR1C1	6805	3E-08	3.372689
202831_at	NM_002083	GPX2	6979	0	3.429494
205328_at	NM_006984	CLDN10	7155	0	3.432973
201468_s_at	NM_000903	NQO1	6118	0	3.467371
201467_s_at	NM_000903	NQO1	6118	0	4.008402
209699_x_at	NM_001354	AKR1C2	15722	1.6E-07	4.214368
217626_at	BF508244	AKR1C1	6805	8E-08	5.286915
205623_at	NM_000691	ALDH3A1	6081	0	6.067625
202435_s_at	NM_000104	CYP1B1	6118	9.61E-06	7.096588
202436_s_at	NM_000104	CYP1B1	6118	2.96E-06	14.65085
202437_s_at	NM_000104	CYP1B1	6118	5.5E-07	25.18444

FIG. 12
(cont'd.)